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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/623,304A

DATE: 05/06/2002
TIME: 14:23:25

Input Set : A:\185124-1.app
Output Set: N:\CRF3\05062002\I623304A.raw

```
 3 <110> APPLICANT: Silvia, Christopher
 4        Yu, Weifeng
 5        ICAgen, Inc.
 7 <120> TITLE OF INVENTION: Identification and Expression of Human Kir5.1
 9 <130> FILE REFERENCE: 018512-000410US
11 <140> CURRENT APPLICATION NUMBER: US 09/623,304A
12 <141> CURRENT FILING DATE: 2001-02-21
14 <150> PRIOR APPLICATION NUMBER: US 60/076,612
15 <151> PRIOR FILING DATE: 1998-03-03
17 <150> PRIOR APPLICATION NUMBER: WO PCT/US99/04549
18 <151> PRIOR FILING DATE: 1999-03-02
20 <160> NUMBER OF SEQ ID NOS: 4
22 <170> SOFTWARE: PatentIn Ver. 2.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 383
26 <212> TYPE: PRT
27 <213> ORGANISM: Homo sapiens
29 <220> FEATURE:
30 <223> OTHER INFORMATION: human Kir5.1 alpha subunit monomer of inward
31        rectifier potassium channel
33 <220> FEATURE:
34 <221> NAME/KEY: PEPTIDE
35 <222> LOCATION: (351)..(383)
36 <223> OTHER INFORMATION: tail region
38 <220> FEATURE:
39 <221> NAME/KEY: MOD_RES
40 <222> LOCATION: (303)
41 <223> OTHER INFORMATION: Xaa = Lys or Glu
43 <400> SEQUENCE: 1
44 Met Ser Tyr Tyr Gly Ser Ser Tyr His Ile Ile Asn Ala Asp Ala Lys
45   1               5                  10                  15
46 Tyr Pro Gly Tyr Pro Pro Glu His Ile Ile Ala Glu Lys Arg Arg Ala
47               20                  25                  30
48 Arg Arg Arg Leu Leu His Lys Asp Gly Ser Cys Asn Val Tyr Phe Lys
49           35                  40                  45
50 His Ile Phe Gly Glu Trp Gly Ser Tyr Val Val Asp Ile Phe Thr Thr
51       50                  55                  60
52 Leu Val Asp Thr Lys Trp Arg His Met Phe Val Ile Phe Ser Leu Ser
53   65                  70                  75                  80
54 Tyr Ile Leu Ser Trp Leu Ile Phe Gly Ser Val Phe Trp Leu Ile Ala
55                   85                  90                  95
56 Phe His His Gly Asp Leu Leu Asn Asp Pro Asp Ile Thr Pro Cys Val
57               100                 105                 110
```

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```
 58 Asp Asn Val His Ser Phe Thr Gly Ala Phe Leu Phe Ser Leu Glu Thr
 59          115                 120                 125
 60 Gln Thr Thr Ile Gly Tyr Gly Tyr Arg Cys Val Thr Glu Glu Cys Ser
 61      130                 135                 140
 62 Val Ala Val Leu Met Val Ile Leu Gln Ser Ile Leu Ser Cys Ile Ile
 63 145                 150                 155                 160
 64 Asn Thr Phe Ile Ile Gly Ala Ala Leu Ala Lys Met Ala Thr Ala Arg
 65                  165                 170                 175
 66 Lys Arg Ala Gln Thr Ile Arg Phe Ser Tyr Phe Ala Leu Ile Gly Met
 67              180                 185                 190
 68 Arg Asp Gly Lys Leu Cys Leu Met Trp Arg Ile Gly Asp Phe Arg Pro
 69          195                 200                 205
 70 Asn His Val Val Glu Gly Thr Val Arg Ala Gln Leu Leu Arg Tyr Thr
 71      210                 215                 220
 72 Glu Asp Ser Glu Gly Arg Met Thr Met Ala Phe Lys Asp Leu Lys Leu
 73 225                 230                 235                 240
 74 Val Asn Asp Gln Ile Ile Leu Val Thr Pro Val Thr Ile Val His Glu
 75                  245                 250                 255
 76 Ile Asp His Glu Ser Pro Leu Tyr Ala Leu Asp Arg Lys Ala Val Ala
 77          260                 265                 270
 78 Lys Asp Asn Phe Glu Ile Leu Val Thr Phe Ile Tyr Thr Gly Asp Ser
 79          275                 280                 285
W--> 80 Thr Gly Thr Ser His Gln Ser Arg Ser Ser Tyr Val Pro Arg Xaa Ile
 81      290                 295                 300
 82 Leu Trp Gly His Arg Phe Asn Asp Val Leu Glu Val Lys Arg Lys Tyr
 83 305                 310                 315                 320
 84 Tyr Lys Val Asn Cys Leu Gln Phe Glu Gly Ser Val Glu Val Tyr Ala
 85                  325                 330                 335  .
 86 Pro Phe Cys Ser Ala Lys Gln Leu Asp Trp Lys Asp Gln Gln Leu His
 87          340                 345                 350
 88 Ile Glu Lys Ala Pro Pro Val Arg Glu Ser Cys Thr Ser Asp Thr Lys
 89          355                 360                 365
 90 Ala Arg Arg Arg Ser Phe Ser Ala Val Ala Ile Val Ser Ser Trp
 91      370                 375                 380
 94 <210> SEQ ID NO: 2
 95 <211> LENGTH: 1509
 96 <212> TYPE: DNA
 97 <213> ORGANISM: Homo sapiens
 99 <220> FEATURE:
100 <223> OTHER INFORMATION: human Kir5.1 alpha subunit monomer of inward
101       rectifier potassium channel
103 <220> FEATURE:
104 <221> NAME/KEY: CDS
105 <222> LOCATION: (46)..(1197)
106 <223> OTHER INFORMATION: human Kir5.1 alpha subunit
108 <220> FEATURE:
109 <221> NAME/KEY: unsure
110 <222> LOCATION: (1279)
111 <223> OTHER INFORMATION: n = a, g, c or t
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RAW SEQUENCE LISTING   DATE: 05/06/2002
PATENT APPLICATION: US/09/623,304A   TIME: 14:23:25

Input Set : A:\185124-1.app
Output Set: N:\CRF3\05062002\I623304A.raw

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113 <400> SEQUENCE: 2
114 ttactactac aaaactcacc tggatcccta agggcacagc aaagaatgag ctattacggc 60
115 agcagctatc atattatcaa tgcggacgca aaatacccag gctacccgcc agagcacatt 120
116 atagctgaga agagaagagc aagaagacga ttacttcaca aagatggcag ctgtaatgtc 180
117 tacttcaagc acattttgg agaatgggga agctatgtgg ttgacatctt caccactctt 240
118 gtggacacca agtggcgcca tatgtttgtg atattttctt tatcttatat tctctcgtgg 300
119 ttgatatttg gctctgtctt ttggctcata gcctttcatc atggcgatct attaaatgat 360
120 ccagacatca caccttgtgt tgacaacgtc cattctttca cagggccttt tttgttctcc 420
121 ctagagaccc aaaccaccat aggatatggt tatcgctgtg ttactgaaga atgttctgtg 480
122 gccgtgctca tggtgatcct ccagtccatc ttaagttgca tcataaatac ctttatcatt 540
123 ggagctgcct tggccaaaat ggcaactgct cgaaagagag cccaaaccat tcgtttcagc 600
124 tactttgcac ttataggtat gagagatggg aagctttgcc tcatgtggcg cattggtgat 660
125 tttcggccaa accacgtggt agaaggaaca gttagagccc aacttctccg ctatacagaa 720
126 gacagtgaag ggaggatgac gatggcattt aaagacctca aattagtcaa cgaccaaatc 780
127 atcctggtca ccccggtaac tattgtccat gaaattgacc atgagagccc tctgtatgcc 840
128 cttgaccgca aagcagtagc caaagataac tttgagattt tggtgacatt tatctatact 900
129 ggtgattcca ctggaacatc tcaccaatct agaagctcct atgttccccg araaattctc 960
130 tggggccata ggtttaatga tgtcttggaa gttaagagga agtattacaa agtgaactgc 1020
131 ttacagtttg aaggaagtgt ggaagtatat gccccctttt gcagtgccaa gcaattggac 1080
132 tggaaagacc agcagctcca catagaaaaa gcaccaccag ttcgagaatc ctgcacgtcg 1140
133 gacaccaagg cgagacgaag gtcatttagt gcagttgcca ttgtcagcag ctggtgaaaa 1200
134 ccctgaggag accaccactt cgccacaca tgaatatagg gaaacacctt atcagaaagc 1260
```
W--> 135 **tctccctgac tttaaacang aatcctctgt wgaatcccaa atgttagtcc taaaattgca 1320**
```
136 attatgaggg ctaccactga atcattttat ctttcagcca atcaagtcgt tgtaaacgtg 1380
137 gcttttttga aagtgttatg gctatgtttt atgatgatgc tgggtaagta gagtaagtta 1440
138 aacttggtaa aagataatct aaaaattcca tagttctcag ttattaaaat ttttcttgtt 1500
139 ccggaattc                                                      1509
141 <210> SEQ ID NO: 3
142 <211> LENGTH: 24
143 <212> TYPE: DNA
144 <213> ORGANISM: Artificial Sequence
146 <220> FEATURE:
147 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
149 <400> SEQUENCE: 3
150 cctaagggca cagcaaagaa tgag                                      24
152 <210> SEQ ID NO: 4
153 <211> LENGTH: 20
154 <212> TYPE: DNA
155 <213> ORGANISM: Artificial Sequence
157 <220> FEATURE:
158 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
160 <400> SEQUENCE: 4
161 gtgtggcgaa agtggtggtc                                           20
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 05/06/2002
PATENT APPLICATION: US/09/623,304A   TIME: 14:23:26

Input Set : A:\185124-1.app
Output Set: N:\CRF3\05062002\I623304A.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 303
Seq#:2; N Pos. 1279

VERIFICATION SUMMARY　　　　　　　　　DATE: 05/06/2002
PATENT APPLICATION:　**US/09/623,304A**　　　TIME: 14:23:26

Input Set : **A:\185124-1.app**
Output Set: **N:\CRF3\05062002\I623304A.raw**

L:80 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:288
L:135 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:1260